

AMENDMENTS TO THE SPECIFICATION:

Please amend the paragraph on page 6, lines 13-16 as follows:

A preferred xylanase is the *Thermomyces* xylanase of SwissProt Q43097 (of which the mature peptide corresponds to amino-acids-31-225 amino acids 1-195 of SEQ ID NO: 14), or analogues thereof as defined in (iv)-(ix) above. This xylanase is also described in WO96/23062, and it has a T_m at pH 7.0 of 75.0°C (see Example 6).

Please amend the paragraph on page 8, lines 7-12 as follows:

In another embodiment, the polypeptide is derived from a fungus of the genus *Thermoascus*, for example the species *Thermoascus aurantiacus*, such as the strain *Thermoascus aurantiacus* CGMCC No. 0670, e.g., a polypeptide with the amino acid sequence of amino acids 1-335, or 31-335 -30-305 or 1-305 of SEQ ID NO:2. This endoglucanase (also having endo-1,3(4)-beta-glucanase activity) is thermostable as disclosed in the experimental part hereof (T_m of 77.5°C).

Please amend the paragraph on page 13, lines 13-18 as follows:

Preferred thermostable phytases for use according to the invention are the various thermostable variants of the *Peniophora lycii* phytase (mature peptide corresponding to amino acids-31-225 amino acids 1-409 of SEQ ID NO: 15). These thermostable variants are disclosed in DK patent applications no. 2002 00193 and 2002 01449, filed 08.02.2002. and 30.09.2002. respectively. The thermostable variants have a degree of identity to amino-acids-31-225 amino acids 1-409 of SEQ ID NO: 15 of at least 75%.

Please amend the paragraph on page 29, lines 15-25 as follows:

A composition comprising i) at least one polypeptide having xylanase activity, the polypeptide being a family 11 glycoside hydrolase; and ii) at least one polypeptide having endoglucanase activity, the polypeptide comprising (a) an amino acid sequence of at least 75 % identity to amino acids 1-to-335, or 31-to-335 -30-305 or 1-305 of SEQ ID NO:2, and/or wherein the polypeptide is (b) encoded by a nucleic acid sequence which hybridizes under low

stringency conditions with (i) the mature endoglucanase encoding part of the plasmid contained in Escherichia coli DSM 14541, (ii) nucleotides ~~4 to 1008, or 90 to 1008~~ 1 to 1008 or 91 to 1008 of SEQ ID NO:1, (iii) a subsequence of (i) or (ii) of at least 100 nucleotides, or (iv) a complementary strand of (i), (ii) or (iii); (c) a variant of the polypeptide having the amino acid sequence of SEQ ID NO:2 comprising a substitution, deletion, and/or insertion of one or more amino acids, (d) an allelic variant of (a) or (b), or (e) a fragment of (a), (b), or (d) that has endoglucanase activity;

Please amend the paragraph on page 41, lines 1-4 as follows:

Sequence analysis of the cDNA clone showed that the sequence contains a coding region of 1005 nucleotides (SEQ ID NO: 1). The translation product having SEQ ID NO: 2 is 335 amino acids in length. Expectedly, amino acid residues ~~4 to 30~~ 30 to 1 constitute a signal-peptide part, and amino acid residues ~~31 to 335~~ constitutes 1 to 305 constitute the catalytic domain.